

SEQUENCE LISTING

<110> COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION

<120> Polyphenol oxidase genes from banana, lettuce, tobacco and  
pineapple

<140>

<141>

<150> US 08/976, 222

<151> 1997-11-21

<150> PCT/AU98/00362

<151> 1998-05-19

<150> AU PP3898

<151> 1995-05-23

<150> AU PP6849

<151> 1997-05-19

<150> AU PP5600

<151> 1995-09-26

<160> 49

<170> PatentIn Ver. 2.0

<210> 1

<211> 582

<212> DNA

<213> banana

<220>

<221> CDS

<222> (1)..(582)

<400> 1

cac tgt gcg tat tgt gat ggc gcc tac gac cag atc ggc ttc ccc aac 48  
His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asn  
1 5 10 15

ctc gag ctc caa gtc cac aac tcc tgg ctc ttc ttc cct tgg cac cgc 96  
Leu Glu Leu Gln Val His Asn Ser Trp Leu Phe Phe Pro Trp His Arg  
20 25 30

ttc tac ctc tac ttc cac gag agg atc ctc gga aag ctc ata ggc gac 144  
Phe Tyr Leu Tyr Phe His Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp  
35 40 45

gac act ttc gcc ctc cct ttc tgg aac tgg gac gcg ccc ggc ggc atg 192  
Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met

50	55	60	
aag ctg ccg tgc atc tac gcc gac cct tgc tcc tgc ctc tat gac aag			240
Lys Leu Pro Ser Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys			
65	70	75	80
ttt cgc gac gcc aag cac cag ccg cca gtc ctc gtc gac ctc gac tac			288
Phe Arg Asp Ala Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr			
	85	90	95
aac gga acc gac cct agt ttc acc gac gca gag cag atc gat cag aac			336
Asn Gly Thr Asp Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn			
	100	105	110
ctc aag atc atg tac cgg cag gtg atc tcc aac ggc aag acg ccg ttg			384
Leu Lys Ile Met Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu			
	115	120	125
ctc ttc tta ggc tgc gct tac cgt gcc ggc gac aac cca aac ccc ggc			432
Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly			
	130	135	140
gcg ggc tgc ctc gag aac ata cca cac ggc ccc gtc cac ggg tgg act			480
Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr			
145	150	155	160
ggc gac aga agc caa ccc aat ctc gag gac atg ggc aac ttc tac tcc			528
Gly Asp Arg Ser Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser			
	165	170	175
gcg ggg cgc gac cct atc ttc ttc gcc cac cat tca aat gtc gat cgc			576
Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg			
	180	185	190
atg tgg			582
Met Trp			

<210> 2  
 <211> 194  
 <212> PRT  
 <213> banana

<400> 2  
 His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asn  
 1 5 10 15

Leu Glu Leu Gln Val His Asn Ser Trp Leu Phe Phe Pro Trp His Arg

20	25	30
Phe Tyr Leu Tyr Phe His Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp		
35	40	45
Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met		
50	55	60
Lys Leu Pro Ser Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys		
65	70	75 80
Phe Arg Asp Ala Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr		
85	90	95
Asn Gly Thr Asp Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn		
100	105	110
Leu Lys Ile Met Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu		
115	120	125
Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly		
130	135	140
Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr		
145	150	155 160
Gly Asp Arg Ser Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser		
165	170	175
Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg		
180	185	190
Met Trp		

<210> 3

<211> 426

<212> DNA

<213> banana

<220>

<221> CDS

<222> (1)..(426)

<400> 3

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Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Lys Leu Pro Ser  
 1 5 10 15  
 atc tac gcc gac cct tcg tcc tcg ctc tat gac aag ttt cgc gac gcc 96  
 Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys Phe Arg Asp Ala  
 20 25 30  
 aag cac cag ccg ccg gtc ctc gtc gac ctc gac tac aac gga acc gac 144  
 Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp  
 35 40 45  
 cct agt ttc acc gac gca gag cag atc gat cag aac ctc aag atc atg 192  
 Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn Leu Lys Ile Met  
 50 55 60  
 tac cgg cag gtg atc tcc aac ggc aag acg ccg ttg ctc ttc tta ggc 240  
 Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu Leu Phe Leu Gly  
 65 70 75 80  
 tcg gct tac cgt gcc ggc gac aac cca aac ccc ggc gcg ggc tcg ctc 288  
 Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly Ala Gly Ser Leu  
 85 90 95  
 gag aac ata cca cac ggc ccc gtc cac ggg tgg act ggc gac aga agc 336  
 Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr Gly Asp Arg Ser  
 100 105 110  
 caa ccc aat ctc gag gac atg ggc aac ttc tac tcc gcg ggg cgc gac 384  
 Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser Ala Gly Arg Asp  
 115 120 125  
 cct atc ttc ttc gcc cac cat tca aat gtc gat agc atg tgg 426  
 Pro Ile Phe Phe Ala His His Ser Asn Val Asp Ser Met Trp  
 130 135 140

<210> 4

<211> 142

<212> PRT

<213> banana

<400> 4

Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Lys Leu Pro Ser  
 1 5 10 15  
 Ile Tyr Ala Asp Pro Ser Ser Ser Leu Tyr Asp Lys Phe Arg Asp Ala  
 20 25 30

Lys His Gln Pro Pro Val Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp  
35 40 45

Pro Ser Phe Thr Asp Ala Glu Gln Ile Asp Gln Asn Leu Lys Ile Met  
50 55 60

Tyr Arg Gln Val Ile Ser Asn Gly Lys Thr Pro Leu Leu Phe Leu Gly  
65 70 75 80

Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro Gly Ala Gly Ser Leu  
85 90 95

Glu Asn Ile Pro His Gly Pro Val His Gly Trp Thr Gly Asp Arg Ser  
100 105 110

Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr Ser Ala Gly Arg Asp  
115 120 125

Pro Ile Phe Phe Ala His His Ser Asn Val Asp Ser Met Trp  
130 135 140

<210> 5

<211> 925

<212> DNA

<213> banana

<220>

<221> CDS

<222> (2)..(853)

<400> 5

g ttg ctc ttc tta ggc tcg gct tac cgt gcc ggc gac aac cca aac ccc 49

Leu Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro

1 5 10 15

ggc gcg ggc tcg ctc gag aac ata cca cac ggc ccc gtc cac ggg tgg 97

Gly Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp

20 25 30

act ggc gac aga aac caa ccc aat ctc gag gac atg ggc aac ttc tac 145

Thr Gly Asp Arg Asn Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr

35 40 45

tcc gcg ggg cgc gac cct atc ttc ttc gcc cac cat tca aac gtc gac 193

Ser Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp

50	55	60	
cgc atg tgg tac ttg tgg aag aag ctc ggc ggg aag cat cag gac ttt			241
Arg Met Trp Tyr Leu Trp Lys Lys Leu Gly Gly Lys His Gln Asp Phe			
65	70	75	80
aac gat aag gac tgg ctc aac acc acc ttc ctc ttc tac gac gag aat			289
Asn Asp Lys Asp Trp Leu Asn Thr Thr Phe Leu Phe Tyr Asp Glu Asn			
	85	90	95
gct gac tta gtt cga gtc acc ctc aag gac tgc ttg cag ccg gag tgg			337
Ala Asp Leu Val Arg Val Thr Leu Lys Asp Cys Leu Gln Pro Glu Trp			
100	105	110	
ctt cgt tac gat tac caa gac gtc gag atc ccg tgg ctg aag acc cgg			385
Leu Arg Tyr Asp Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Thr Arg			
115	120	125	
ccg act ccc aaa gcc ttg aag gcg cag aaa acc gca gcg aaa aca ctg			433
Pro Thr Pro Lys Ala Leu Lys Ala Gln Lys Thr Ala Ala Lys Thr Leu			
130	135	140	
aaa gct aca gca gag acg ccg ttc ccg gtg acg ctg caa tcc gcg gtg			481
Lys Ala Thr Ala Glu Thr Pro Phe Pro Val Thr Leu Gln Ser Ala Val			
145	150	155	160
agc acg acg gtg agg agg ccc aag gta tcg agg agc ggc aag gag aag			529
Ser Thr Thr Val Arg Arg Pro Lys Val Ser Arg Ser Gly Lys Glu Lys			
165	170	175	
gaa gag gaa gag gag gtc ctc atc gtg gag ggg atc gag ttc gac cgc			577
Glu Glu Glu Glu Glu Val Leu Ile Val Glu Gly Ile Glu Phe Asp Arg			
180	185	190	
gac tac ttc ata aag ttc gac gtc ttc gtg aac gcc acc gag ggt gag			625
Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Glu			
195	200	205	
ggc atc acg ccg ggc gcc agc gag ttc gcg ggc agc ttc gtc aac gtc			673
Gly Ile Thr Pro Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val			
210	215	220	
ccg cac aag cac aag cac agc aag aag gag aag aag ctg aag acg agg			721
Pro His Lys His Lys His Ser Lys Lys Glu Lys Lys Leu Lys Thr Arg			
225	230	235	240
ctc tgc ctg ggg atc act gac ctg ctc gag gac atc ggg gcg gag gac			769
Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp			

245	250	255	
gac gac agc gtg ctc gtc acc atc gtc ccg aaa gcc gga aag ggc aag 817			
Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys			
260	265	270	
gtg tcg gtc gcc ggc ctc cgc atc gat ttc cca aat tgaagtaata 863			
Val Ser Val Ala Gly Leu Arg Ile Asp Phe Pro Asn			
275	280		
ctatatattt ctactaccta tcaaggaaaa taaaagccgc accatcgtaa caaaaaaaaaa 923			
aa 925			
<210> 6			
<211> 284			
<212> PRT			
<213> banana			
<400> 6			
Leu Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Asn Pro Asn Pro			
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Gly Ala Gly Ser Leu Glu Asn Ile Pro His Gly Pro Val His Gly Trp			
20	25	30	
Thr Gly Asp Arg Asn Gln Pro Asn Leu Glu Asp Met Gly Asn Phe Tyr			
35	40	45	
Ser Ala Gly Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp			
50	55	60	
Arg Met Trp Tyr Leu Trp Lys Lys Leu Gly Gly Lys His Gln Asp Phe			
65	70	75	80
Asn Asp Lys Asp Trp Leu Asn Thr Thr Phe Leu Phe Tyr Asp Glu Asn			
85	90	95	
Ala Asp Leu Val Arg Val Thr Leu Lys Asp Cys Leu Gln Pro Glu Trp			
100	105	110	
Leu Arg Tyr Asp Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Thr Arg			
115	120	125	
Pro Thr Pro Lys Ala Leu Lys Ala Gln Lys Thr Ala Ala Lys Thr Leu			
130	135	140	

Lys Ala Thr Ala Glu Thr Pro Phe Pro Val Thr Leu Gln Ser Ala Val  
145 150 155 160

Ser Thr Thr Val Arg Arg Pro Lys Val Ser Arg Ser Gly Lys Glu Lys  
165 170 175

Glu Glu Glu Glu Glu Val Leu Ile Val Glu Gly Ile Glu Phe Asp Arg  
180 185 190

Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Glu  
195 200 205

Gly Ile Thr Pro Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val  
210 215 220

Pro His Lys His Lys His Ser Lys Lys Glu Lys Lys Leu Lys Thr Arg  
225 230 235 240

Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp  
245 250 255

Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys  
260 265 270

Val Ser Val Ala Gly Leu Arg Ile Asp Phe Pro Asn  
275 280

<210> 7

<211> 960

<212> DNA

<213> banana

<220>

<221> CDS

<222> (2)..(853)

<400> 7

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Leu Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asn Pro  
1 5 10 15

ggc gcg gga tcc atc gag aac atg ccg cac aac aac gtg cac ttg tgg 97  
Gly Ala Gly Ser Ile Glu Asn Met Pro His Asn Asn Val His Leu Trp  
20 25 30

acc ggc gac cgc acc cag ccc aac ttc gag aac atg ggc acc ttc tac 145



Thr Gly Asp Arg Thr Gln Pro Asn Phe Glu Asn Met Gly Thr Phe Tyr	
35 40 45	
gcg gcg gcg cgc gac ccc atc ttc ttc gcc cac cac gcc aac atc gac	193
Ala Ala Ala Arg Asp Pro Ile Phe Phe Ala His His Ala Asn Ile Asp	
50 55 60	
cga atg tgg tac ctg tgg aag aag ctc agc agg aag cac cag gac ttc	241
Arg Met Trp Tyr Leu Trp Lys Lys Leu Ser Arg Lys His Gln Asp Phe	
65 70 75 80	
aat gac tcg gac tgg ctc aaa gct tcc ttc ctc ttc tac gac gag aac	289
Asn Asp Ser Asp Trp Leu Lys Ala Ser Phe Leu Phe Tyr Asp Glu Asn	
85 90 95	
gcc gac tta gtt cgg gtc acg gtc aag gac tgc ttg gag acc gag tgg	337
Ala Asp Leu Val Arg Val Thr Val Lys Asp Cys Leu Glu Thr Glu Trp	
100 105 110	
ctg cgc tac acg tac caa gac gtg aag atc cca tgg gcg aac acc cga	385
Leu Arg Tyr Thr Tyr Gln Asp Val Lys Ile Pro Trp Ala Asn Thr Arg	
115 120 125	
ccg act ccc aag ctc gcc aag gcg agg aaa gcc ggc agc aga tcg ctg	433
Pro Thr Pro Lys Leu Ala Lys Ala Arg Lys Ala Gly Ser Arg Ser Leu	
130 135 140	
aaa gcc acc gcg gag gtg cag ttc cct gtg acg ctg gaa tcc ccg gtc	481
Lys Ala Thr Ala Glu Val Gln Phe Pro Val Thr Leu Glu Ser Pro Val	
145 150 155 160	
aaa gtg acg gtg aag agg ccc aag gtg ggg agg agc ggc aag gag aag	529
Lys Val Thr Val Lys Arg Pro Lys Val Gly Arg Ser Gly Lys Glu Lys	
165 170 175	
gaa gat gag gag gag ata ctc ata gtg gag ggg atc gag ttc gac cgc	577
Glu Asp Glu Glu Glu Ile Leu Ile Val Glu Gly Ile Glu Phe Asp Arg	
180 185 190	
gac tac ttc atc aag ttc gac gtc ttc gtg aac gcg acg gag ggc gac	625
Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Asp	
195 200 205	
ggc atc acg gcc ggg gcc agt gag ttc gcc ggc agc ttc gtg aac gtc	673
Gly Ile Thr Ala Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val	
210 215 220	

ccg cac aag cac aag cac cgc aag gat gag aat aag ctg aag acg agg 721  
 Pro His Lys His Lys His Arg Lys Asp Glu Asn Lys Leu Lys Thr Arg  
 225 230 235 240

ctg tgt ctg gga atc acc gac ctg ctc gag gac atc ggc gcg gag gac 769  
 Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp  
 245 250 255

gac gac agc gtg ctc gtc acc atc gtg ccg aag gca ggc aaa gga aag 817  
 Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys  
 260 265 270

gtg tcc gtc ggc ggt ctt cgg att gac ttt tcc aag tgaggaaata 863  
 Val Ser Val Gly Gly Leu Arg Ile Asp Phe Ser Lys  
 275 280

aaagaattca cgtgccgtgc ctgctttcaa tgtacgaata aaataagagt gcatcatcac 923

cgaccatggt tctacttttaa aaaaaaaaaa aaaaaaa 960

<210> 8

<211> 284

<212> PRT

<213> banana

<400> 8

Leu Leu Phe Leu Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asn Pro  
 1 5 10 15

Gly Ala Gly Ser Ile Glu Asn Met Pro His Asn Asn Val His Leu Trp  
 20 25 30

Thr Gly Asp Arg Thr Gln Pro Asn Phe Glu Asn Met Gly Thr Phe Tyr  
 35 40 45

Ala Ala Ala Arg Asp Pro Ile Phe Phe Ala His His Ala Asn Ile Asp  
 50 55 60

Arg Met Trp Tyr Leu Trp Lys Lys Leu Ser Arg Lys His Gln Asp Phe  
 65 70 75 80

Asn Asp Ser Asp Trp Leu Lys Ala Ser Phe Leu Phe Tyr Asp Glu Asn  
 85 90 95

Ala Asp Leu Val Arg Val Thr Val Lys Asp Cys Leu Glu Thr Glu Trp  
 100 105 110

Leu Arg Tyr Thr Tyr Gln Asp Val Lys Ile Pro Trp Ala Asn Thr Arg  
115 120 125

Pro Thr Pro Lys Leu Ala Lys Ala Arg Lys Ala Gly Ser Arg Ser Leu  
130 135 140

Lys Ala Thr Ala Glu Val Gln Phe Pro Val Thr Leu Glu Ser Pro Val  
145 150 155 160

Lys Val Thr Val Lys Arg Pro Lys Val Gly Arg Ser Gly Lys Glu Lys  
165 170 175

Glu Asp Glu Glu Glu Ile Leu Ile Val Glu Gly Ile Glu Phe Asp Arg  
180 185 190

Asp Tyr Phe Ile Lys Phe Asp Val Phe Val Asn Ala Thr Glu Gly Asp  
195 200 205

Gly Ile Thr Ala Gly Ala Ser Glu Phe Ala Gly Ser Phe Val Asn Val  
210 215 220

Pro His Lys His Lys His Arg Lys Asp Glu Asn Lys Leu Lys Thr Arg  
225 230 235 240

Leu Cys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp  
245 250 255

Asp Asp Ser Val Leu Val Thr Ile Val Pro Lys Ala Gly Lys Gly Lys  
260 265 270

Val Ser Val Gly Gly Leu Arg Ile Asp Phe Ser Lys  
275 280

<210> 9

<211> 545

<212> DNA

<213> tobacco

<220>

<221> CDS

<222> (1)..(543)

<400> 9

gat ccg acg ttt gcg ttg cca tat tgg aac tgg gat cat cca aag ggc 48  
Asp Pro Thr Phe Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly  
1 5 10 15

atg cgt ttg cca cac atg ttt gat caa cca aac gtg tac cct gat ctt	96
Met Arg Leu Pro His Met Phe Asp Gln Pro Asn Val Tyr Pro Asp Leu	
20 25 30	
tac gat cca aga cgt aac caa gaa cac cgc ggt tct gta atc atg gac	144
Tyr Asp Pro Arg Arg Asn Gln Glu His Arg Gly Ser Val Ile Met Asp	
35 40 45	
ctt ggt cat ttt ggt caa gac gtg aaa gga act gac ttg caa atg atg	192
Leu Gly His Phe Gly Gln Asp Val Lys Gly Thr Asp Leu Gln Met Met	
50 55 60	
agc aat aac ctt act cta atg tat cgt caa atg att acc aat tca cca	240
Ser Asn Asn Leu Thr Leu Met Tyr Arg Gln Met Ile Thr Asn Ser Pro	
65 70 75 80	
tgt cca caa ctc ttt ttc ggt aag cca tat tgt acg gaa gtt gga ccc	288
Cys Pro Gln Leu Phe Phe Gly Lys Pro Tyr Cys Thr Glu Val Gly Pro	
85 90 95	
aaa cca ggg cag gga gct att gaa aac atc cct cat act cct gtc cac	336
Lys Pro Gly Gln Gly Ala Ile Glu Asn Ile Pro His Thr Pro Val His	
100 105 110	
att tgg gtt ggt agt aag cct aat gag aat aac tgt aaa aac ggt gaa	384
Ile Trp Val Gly Ser Lys Pro Asn Glu Asn Asn Cys Lys Asn Gly Glu	
115 120 125	
gat atg gga aat ttc tat tca gct ggt aag gat cct gct ttc tat agt	432
Asp Met Gly Asn Phe Tyr Ser Ala Gly Lys Asp Pro Ala Phe Tyr Ser	
130 135 140	
cac cat gca aat gta gat cgc atg tgg aca ata tgg aaa aca tta gga	480
His His Ala Asn Val Asp Arg Met Trp Thr Ile Trp Lys Thr Leu Gly	
145 150 155 160	
gga aaa cgc aag gac atc aac aag cca gat tat ttg aac act gag ttc	528
Gly Lys Arg Lys Asp Ile Asn Lys Pro Asp Tyr Leu Asn Thr Glu Phe	
165 170 175	
ttt ttc tac gac gaa aa	545
Phe Phe Tyr Asp Glu	
180	

<210> 10

<211> 181

<212> PRT

<213> tobacco

<400> 10

Asp Pro Thr Phe Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly  
1 5 10 15

Met Arg Leu Pro His Met Phe Asp Gln Pro Asn Val Tyr Pro Asp Leu  
20 25 30

Tyr Asp Pro Arg Arg Asn Gln Glu His Arg Gly Ser Val Ile Met Asp  
35 40 45

Leu Gly His Phe Gly Gln Asp Val Lys Gly Thr Asp Leu Gln Met Met  
50 55 60

Ser Asn Asn Leu Thr Leu Met Tyr Arg Gln Met Ile Thr Asn Ser Pro  
65 70 75 80

Cys Pro Gln Leu Phe Phe Gly Lys Pro Tyr Cys Thr Glu Val Gly Pro  
85 90 95

Lys Pro Gly Gln Gly Ala Ile Glu Asn Ile Pro His Thr Pro Val His  
100 105 110

Ile Trp Val Gly Ser Lys Pro Asn Glu Asn Asn Cys Lys Asp Gly Glu  
115 120 125

Asp Met Gly Asn Phe Tyr Ser Ala Gly Lys Asp Pro Ala Phe Tyr Ser  
130 135 140

His His Ala Asn Val Asp Arg Met Trp Thr Ile Trp Lys Thr Leu Gly  
145 150 155 160

Gly Lys Arg Lys Asp Ile Asn Lys Pro Asp Tyr Leu Asn Thr Glu Phe  
165 170 175

Phe Phe Tyr Asp Glu  
180

<210> 11

<211> 673

<212> DNA

<213> tobacco

<220>

<221> CDS

<222> (3)..(671)

<400> 11

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His Cys Ala Tyr Cys Asn Gly Ala Tyr Lys Ile Gly Gly Lys Glu	
1 5 10 15	
tta caa gtc cat ttc tcg tgg ctt ttt ttc cct ttt cat aga tgg tac	95
Leu Gln Val His Phe Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr	
20 25 30	
ttg tac ttc tat gaa aga atc ttg ggc tct tta att aat gat cct act	143
Leu Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr	
35 40 45	
ttt ggt ttg cca tat tgg aac tgg gac cat cca aag ggc atg cgt ata	191
Phe Gly Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly Met Arg Ile	
50 55 60	
cct ccc atg ttc gat cgt gaa ggg tct tcc ctt tac gac gaa aaa cgt	239
Pro Pro Met Phe Asp Arg Glu Gly Ser Ser Leu Tyr Asp Glu Lys Arg	
65 70 75	
aac caa agt cac cgt aat gga acc ata att gat ctt ggt cat ttc ggt	287
Asn Gln Ser His Arg Asn Gly Thr Ile Ile Asp Leu Gly His Phe Gly	
80 85 90 95	
caa gaa gtc caa aca act caa ctg cag cag atg act aat aac tta act	335
Gln Glu Val Gln Thr Thr Gln Leu Gln Gln Met Thr Asn Asn Leu Thr	
100 105 110	
ata atg tat cgt caa atg ata act aat gct cct tgc ccc ttg ctc ttc	383
Ile Met Tyr Arg Gln Met Ile Thr Asn Ala Pro Cys Pro Leu Leu Phe	
115 120 125	
ttt ggt cag cct tac cct cta gga act gat ccc agt cca ggg atg ggc	431
Phe Gly Gln Pro Tyr Pro Leu Gly Thr Asp Pro Ser Pro Gly Met Gly	
130 135 140	
act att gaa aac atc cct cat act cct gtc cac att tgg gtt ggt agt	479
Thr Ile Glu Asn Ile Pro His Thr Pro Val His Ile Trp Val Gly Ser	
145 150 155	
agg ctt gat gag aat aat acg aaa cac ggt gag gat atg ggt aat ttt	527
Arg Leu Asp Glu Asn Asn Thr Lys His Gly Glu Asp Met Gly Asn Phe	
160 165 170 175	

tac tcg gcc ggt tta gac ccg ctt ttc tat tcc cat cac gcc aat gtg 575  
Tyr Ser Ala Gly Leu Asp Pro Leu Phe Tyr Ser His His Ala Asn Val  
180 185 190

gac cgg atg tgg tcc gag tgg aaa gcc tta gga ggg aaa aga agg gat 623  
Asp Arg Met Trp Ser Glu Trp Lys Ala Leu Gly Gly Lys Arg Arg Asp  
195 200 205

ctc acg cac aaa gat tgg ttg aac tcc gag ttc ttt ttc tac gat gaa 671  
Leu Thr His Lys Asp Trp Leu Asn Ser Glu Phe Phe Phe Tyr Asp Glu  
210 215 220

aa 673

<210> 12

<211> 223

<212> PRT

<213> tobacco

<400> 12

His Cys Ala Tyr Cys Asn Gly Ala Tyr Lys Ile Gly Gly Lys Glu Leu  
1 5 10 15

Gln Val His Phe Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr Leu  
20 25 30

Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr Phe  
35 40 45

Gly Leu Pro Tyr Trp Asn Trp Asp His Pro Lys Gly Met Arg Ile Pro  
50 55 60

Pro Met Phe Asp Arg Glu Gly Ser Ser Leu Tyr Asp Glu Lys Arg Asn  
65 70 75 80

Gln Ser His Arg Asn Gly Thr Ile Ile Asp Leu Gly His Phe Gly Gln  
85 90 95

Glu Val Gln Thr Thr Gln Leu Gln Gln Met Thr Asn Asn Leu Thr Ile  
100 105 110

Met Tyr Arg Gln Met Ile Thr Asn Ala Pro Cys Pro Leu Leu Phe Phe  
115 120 125

Gly Gln Pro Tyr Pro Leu Gly Thr Asp Pro Ser Pro Gly Met Gly Thr  
130 135 140

Ile Glu Asn Ile Pro His Thr Pro Val His Ile Trp Val Gly Ser Arg  
145 150 155 160

Leu Asp Glu Asn Asn Thr Lys His Gly Glu Asp Met Gly Asn Phe Tyr  
165 170 175

Ser Ala Gly Leu Asp Pro Leu Phe Tyr Ser His His Ala Asn Val Asp  
180 185 190

Arg Met Trp Ser Glu Trp Lys Ala Leu Gly Gly Lys Arg Arg Asp Leu  
195 200 205

Thr His Lys Asp Trp Leu Asn Ser Glu Phe Phe Phe Tyr Asp Glu  
210 215 220

<210> 13

<211> 685

<212> DNA

<213> tobacco

<220>

<221> CDS

<222> (3)..(683)

<400> 13

tg cat tgt gcg tat tgc aac gat gct tac aca atg ggt gac caa aag 47  
His Cys Ala Tyr Cys Asn Asp Ala Tyr Thr Met Gly Asp Gln Lys  
1 5 10 15

tta caa gtt cac caa tcg tgg ctt ttc ttc ccg ttt cat aga tgg tac 95  
Leu Gln Val His Gln Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr  
20 25 30

ttg tac ttc tac gag aga atc ttg ggc tcc ctc atc gat gat cca act 143  
Leu Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asp Asp Pro Thr  
35 40 45

ttt gct ctg cca tat tgg aac tgg gac cat cca agc ggc atg cgt ttg 191  
Phe Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Ser Gly Met Arg Leu  
50 55 60

cct gct atg ttc gat gtc gaa ggt tct tcc ctc tac gat gca aga cgt 239  
Pro Ala Met Phe Asp Val Glu Gly Ser Ser Leu Tyr Asp Ala Arg Arg  
65 70 75

aat cca cat gtc cgt aat gga acc ata atc gat ctt ggt ttt ttc ggt 287



[illegible]

<210> 14

<211> 227

<212> PRT

<213> tobacco

<400> 14

His Cys Ala Tyr Cys Asn Asp Ala Tyr Thr Met Gly Asp Gln Lys Leu

1                      5                      10                      15  
Gln Val His Gln Ser Trp Leu Phe Phe Pro Phe His Arg Trp Tyr Leu  
                    20                      25                      30  
Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asp Asp Pro Thr Phe  
                    35                      40                      45  
Ala Leu Pro Tyr Trp Asn Trp Asp His Pro Ser Gly Met Arg Leu Pro  
                    50                      55                      60  
Ala Met Phe Asp Val Glu Gly Ser Ser Leu Tyr Asp Ala Arg Arg Asn  
                    65                      70                      75                      80  
Pro His Val Arg Asn Gly Thr Ile Ile Asp Leu Gly Phe Phe Gly Asp  
                    85                      90                      95  
Glu Val Lys Thr Asn Glu Ile Gln Met Ile Thr Asn Asn Leu Ile Leu  
                    100                      105                      110  
Met Tyr Arg Gln Met Ile Thr Asn Ala Pro Cys Pro Leu Leu Phe Phe  
                    115                      120                      125  
Gly Glu Pro Tyr Arg Phe Gly Ser Lys Pro Asn Pro Gly Gln Gly Thr  
                    130                      135                      140  
Ile Glu Asn Ile Pro His Thr Pro Val His Ile Trp Thr Gly Thr Val  
                    145                      150                      155                      160  
Arg Cys Thr Asp Leu Gly Asn Cys Val Pro Ser Tyr Gly Glu Asp Met  
                    165                      170                      175  
Gly Asn Phe Tyr Ser Ala Gly Leu Asp Pro Val Phe Tyr Ser His His  
                    180                      185                      190  
Ala Asn Val Asp Arg Met Trp Asn Glu Trp Lys Ala Leu Gly Gly Lys  
                    195                      200                      205  
Arg Arg Asp Leu Thr Asp Asn Asp Trp Leu Asn Ser Glu Phe Phe Phe  
                    210                      215                      220  
Tyr Asp Glu  
225

<210> 15

<211> 670

<212> DNA

<213> pineapple

<220>

<221> CDS

<222> (3)..(668)

<400> 15

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His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro

1 5 10 15

gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt cct tgg cac 95

Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His

20 25 30

cgg ttc tac ctc tac ttc aac gag cgc ata ctc ggg aaa ctt atc ggc 143

Arg Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly

35 40 45

gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg ccg ggg ggc 191

Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly

50 55 60

atg cag ttc ccg tct atc tac acg gac cct tca tcc tcg cta tat gac 239

Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp

65 70 75

aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att gac ctc gac 287

Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp

80 85 90 95

tac aat ggc acc gat cct acc ttc tcc cct gaa gaa cag att aac cac 335

Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His

100 105 110

aac ctc gcc gtc atg tac cga cag gtg ata tcc agt gga aag aca cca 383

Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro

115 120 125

gag ctg ttt atg ggc tca gcg tac cgc gcc ggt gac cag cct gac ccc 431

Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro

130 135 140

ggc gca ggt tct gta gag cag aag ccg cac ggc ccg gtg cat gtg tgg 479

Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp

145 150 155

aca ggt gat cgc aac cag ccc aat cgc gaa gac atg ggc acg ctc tac 527  
 Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr  
 160 165 170 175

tcg gcg gcg tgg gac ccc gtt ttt ttc gca cac cac ggc aac atc gac 575  
 Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp  
 180 185 190

cgc atg tgg tac gtg tgg agg aac ctt ggc ggc aag cac cgc aac ttc 623  
 Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe  
 195 200 205

acc gac ccc gac tgg ctc aac gcg tcc ttc ctg ttc tac gac gaa aa 670  
 Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu  
 210 215 220

<210> 16

<211> 222

<212> PRT

<213> pineapple

<400> 16

His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asp  
 1 5 10 15

Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His Arg  
 20 25 30

Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp  
 35 40 45

Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met  
 50 55 60

Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp Lys  
 65 70 75 80

Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp Tyr  
 85 90 95

Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His Asn  
 100 105 110

Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro Glu  
 115 120 125

Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro Gly

130	135	140	
Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp Thr			
145	150	155	160
Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr Ser			
	165	170	175
Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp Arg			
	180	185	190
Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe Thr			
	195	200	205
Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu			
	210	215	220

<210> 17  
 <211> 1319  
 <212> DNA  
 <213> pineapple

<220>  
 <221> CDS  
 <222> (1)..(1053)

<400> 17

ttg ccg ttt tgg aat tgg gac gcg ccg ggg ggc atg cag atc ccg gcc	48
Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Gln Ile Pro Ala	
1 5 10 15	
atc tac gcc gac gct tcg tcc ccg ctc tac gac aag ctg cgc aat gcg	96
Ile Tyr Ala Asp Ala Ser Ser Pro Leu Tyr Asp Lys Leu Arg Asn Ala	
20 25 30	
aag cac cag ccg ccg act ttg gtc gac ctc gac tac aac ggc acc gac	144
Lys His Gln Pro Pro Thr Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp	
35 40 45	
ccg acc ttc acc cct gag cag cag atc gcc cac aac ctc acc atc atg	192
Pro Thr Phe Thr Pro Glu Gln Gln Ile Ala His Asn Leu Thr Ile Met	
50 55 60	
tac cga cag gtg ata tcc ggc ggg aag acg ccg gag ttg ttt atg ggc	240
Tyr Arg Gln Val Ile Ser Gly Gly Lys Thr Pro Glu Leu Phe Met Gly	
65 70 75 80	

gcg gcg tac cgc gcg ggc gac gcg cca gac ccg ggc gca ggc act cta	288
Ala Ala Tyr Arg Ala Gly Asp Ala Pro Asp Pro Gly Ala Gly Thr Leu	
85 90 95	
gag ctc gtg ccg cac aac acg atg cat ttg tgg acc ggc gac ccc aac	336
Glu Leu Val Pro His Asn Thr Met His Leu Trp Thr Gly Asp Pro Asn	
100 105 110	
caa ccc aac gac gaa gac atg ggc acg ttc tac gcg gcg gcg cgg gac	384
Gln Pro Asn Asp Glu Asp Met Gly Thr Phe Tyr Ala Ala Ala Arg Asp	
115 120 125	
ccc atc ttc ttc gcc cac cac ggc aac gtc gac cgc atg tgg tac gtg	432
Pro Ile Phe Phe Ala His His Gly Asn Val Asp Arg Met Trp Tyr Val	
130 135 140	
tgg cgg aaa ctc ggg ggc acg cac cgc gat ttc acc gac ccc gac tgg	480
Trp Arg Lys Leu Gly Gly Thr His Arg Asp Phe Thr Asp Pro Asp Trp	
145 150 155 160	
ctc aac gcg tcc ttc ctc ttc tac gac gag aac gcg cag ctc gtc cgc	528
Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn Ala Gln Leu Val Arg	
165 170 175	
gtc aaa gta aag gac tgc ttg agc gcc gac gcg ctg cgg tac acg tac	576
Val Lys Val Lys Asp Cys Leu Ser Ala Asp Ala Leu Arg Tyr Thr Tyr	
180 185 190	
cag gac gtc gac atc ccg tgg atc agt gcg aag ccg acg ccg aag aaa	624
Gln Asp Val Asp Ile Pro Trp Ile Ser Ala Lys Pro Thr Pro Lys Lys	
195 200 205	
aca ccg ggg ggc gct gcg cct tcc acg aca gag gct ata ttt ccg gtg	672
Thr Pro Gly Gly Ala Ala Pro Ser Thr Thr Glu Ala Ile Phe Pro Val	
210 215 220	
gtg ctg gat aag ccg gtg agc tct acg gtg gcg agg ccg aag acg ggg	720
Val Leu Asp Lys Pro Val Ser Ser Thr Val Ala Arg Pro Lys Thr Gly	
225 230 235 240	
agg agt act ggg gag gag gag gtg ttg gtg gtg gag gga atc gag ctg	768
Arg Ser Thr Gly Glu Glu Glu Val Leu Val Val Glu Gly Ile Glu Leu	
245 250 255	
gac aag gac gtg gcc gtg aag ttc gac gtg tat ata aac gcg ccg gac	816
Asp Lys Asp Val Ala Val Lys Phe Asp Val Tyr Ile Asn Ala Pro Asp	
260 265 270	

aac gaa ggg gtg ggg ccg gag gcg agc gag ttc gca ggg agc ttc gtc 864  
 Asn Glu Gly Val Gly Pro Glu Ala Ser Glu Phe Ala Gly Ser Phe Val  
 275 280 285  
  
 cag gtg ccg cac aag cac aag aag ggg aag aag gag aag gcg agg att 912  
 Gln Val Pro His Lys His Lys Lys Gly Lys Lys Glu Lys Ala Arg Ile  
 290 295 300  
  
 aaa acg acg ctc agg ctc ggg ata acg gac ctg ctc gag gac atc ggc 960  
 Lys Thr Thr Leu Arg Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly  
 305 310 315 320  
  
 gcc gag gac gac gag agc gtg ctc gtc acg ctc gtg ccg agg ata ggc 1008  
 Ala Glu Asp Asp Glu Ser Val Leu Val Thr Leu Val Pro Arg Ile Gly  
 325 330 335  
  
 gag ggg ttg gtc aag gtt ggt ggg cta agg atc gat ttc tcc aag 1053  
 Glu Gly Leu Val Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys  
 340 345 350  
  
 tgatcagcag caaattaact atacatgaaa gtaaaaaaaaaa ttgcatttac ctacctatag 1113  
 aagagaataa atgcgtatgt aatctgcccc atttgtcact ttttaatttct cgagcgtggt 1173  
 ctgaatgaga gttgcatgca tgcgcgcagc cataatgcct ggtatagtgt agtagtttag 1233  
 gcgtggatac gtataacgta cgtatgcatg tataaggaat aatgatgagt ttactatgca 1293  
 aaaaaaaaaa aaaaaaaaaa aaaaaa 1319

<210> 18  
 <211> 351  
 <212> PRT  
 <213> pineapple

<400> 18  
 Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met Gln Ile Pro Ala  
 1 5 10 15  
  
 Ile Tyr Ala Asp Ala Ser Ser Pro Leu Tyr Asp Lys Leu Arg Asn Ala  
 20 25 30  
  
 Lys His Gln Pro Pro Thr Leu Val Asp Leu Asp Tyr Asn Gly Thr Asp  
 35 40 45

Pro	Thr	Phe	Thr	Pro	Glu	Gln	Gln	Ile	Ala	His	Asn	Leu	Thr	Ile	Met	50	55	60
Tyr	Arg	Gln	Val	Ile	Ser	Gly	Gly	Lys	Thr	Pro	Glu	Leu	Phe	Met	Gly	65	70	75
Ala	Ala	Tyr	Arg	Ala	Gly	Asp	Ala	Pro	Asp	Pro	Gly	Ala	Gly	Thr	Leu	85	90	95
Glu	Leu	Val	Pro	His	Asn	Thr	Met	His	Leu	Trp	Thr	Gly	Asp	Pro	Asn	100	105	110
Gln	Pro	Asn	Asp	Glu	Asp	Met	Gly	Thr	Phe	Tyr	Ala	Ala	Ala	Arg	Asp	115	120	125
Pro	Ile	Phe	Phe	Ala	His	His	Gly	Asn	Val	Asp	Arg	Met	Trp	Tyr	Val	130	135	140
Trp	Arg	Lys	Leu	Gly	Gly	Thr	His	Arg	Asp	Phe	Thr	Asp	Pro	Asp	Trp	145	150	155
Leu	Asn	Ala	Ser	Phe	Leu	Phe	Tyr	Asp	Glu	Asn	Ala	Gln	Leu	Val	Arg	165	170	175
Val	Lys	Val	Lys	Asp	Cys	Leu	Ser	Ala	Asp	Ala	Leu	Arg	Tyr	Thr	Tyr	180	185	190
Gln	Asp	Val	Asp	Ile	Pro	Trp	Ile	Ser	Ala	Lys	Pro	Thr	Pro	Lys	Lys	195	200	205
Thr	Pro	Gly	Gly	Ala	Ala	Pro	Ser	Thr	Thr	Glu	Ala	Ile	Phe	Pro	Val	210	215	220
Val	Leu	Asp	Lys	Pro	Val	Ser	Ser	Thr	Val	Ala	Arg	Pro	Lys	Thr	Gly	225	230	235
Arg	Ser	Thr	Gly	Glu	Glu	Glu	Val	Leu	Val	Val	Glu	Gly	Ile	Glu	Leu	245	250	255
Asp	Lys	Asp	Val	Ala	Val	Lys	Phe	Asp	Val	Tyr	Ile	Asn	Ala	Pro	Asp	260	265	270
Asn	Glu	Gly	Val	Gly	Pro	Glu	Ala	Ser	Glu	Phe	Ala	Gly	Ser	Phe	Val	275	280	285
Gln	Val	Pro	His	Lys	His	Lys	Lys	Gly	Lys	Lys	Glu	Lys	Ala	Arg	Ile	290	295	300



Lys Thr Thr Leu Arg Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly  
305 310 315 320

Ala Glu Asp Asp Glu Ser Val Leu Val Thr Leu Val Pro Arg Ile Gly  
325 330 335

Glu Gly Leu Val Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys  
340 345 350

<210> 19

<211> 2181

<212> DNA

<213> pineapple

<220>

<221> CDS

<222> (2)..(1858)

<400> 19

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Gly Ile Asp Lys Leu Asp Pro Val Pro Gly Leu Gly Val Phe Thr Met

1 5 10 15

gcc acc ctc tct aaa cta gct tcc caa cca ata aca cct cca ctc tcc 97

Ala Thr Leu Ser Lys Leu Ala Ser Gln Pro Ile Thr Pro Pro Leu Ser

20 25 30

ccg ctc cct cct ttg cat gct cct tct ctc acc aaa agc ttc acc acc 145

Pro Leu Pro Pro Leu His Ala Pro Ser Leu Thr Lys Ser Phe Thr Thr

35 40 45

acc ttc ctc tcc cct gta ggg gtc cca aac cac ccc gtc ata aga tct 193

Thr Phe Leu Ser Pro Val Gly Val Pro Asn His Pro Val Ile Arg Ser

50 55 60

cat gca aat cta agg agc aac aag aga atg ccg aca agc ctg cgg gcc 241

His Ala Asn Leu Arg Ser Asn Lys Arg Met Pro Thr Ser Leu Arg Ala

65 70 75 80

gca tcg ccc gcc gcg acc tac tcc tgg gcc ctc ggc ggg ctt tac ggt 289

Ala Ser Pro Ala Ala Thr Tyr Ser Trp Ala Leu Gly Gly Leu Tyr Gly

85 90 95

gcc acc act ggg ctc ggc ctc aac cgt cga gcg gcc gcc gcc cct atc 337

Ala Thr Thr Gly Leu Gly Leu Asn Arg Arg Ala Ala Ala Ala Pro Ile

100 105 110

ctg gct ccc gac ctc tca act tgt ggg ccg cct gcc gac ctc cct gcc	385
Leu Ala Pro Asp Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala	
115 120 125	
tcc gcc cga ccg aca gtt tgc tgc ccg cca tac caa tcc acc atc atc	433
Ser Ala Arg Pro Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile	
130 135 140	
gac ttc aag ctc ccc ccg cga tct gct ccg ctt cgc gtc ccg cct gcg	481
Asp Phe Lys Leu Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala	
145 150 155 160	
gcc cac ttg gtt gac gcc gac tac ctg gcc aag tat aag aag gcg gtc	529
Ala His Leu Val Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val	
165 170 175	
gag ctc atg agg gcc ctg ccg gcc gac gac ccg cgc aac ttc gta cag	577
Glu Leu Met Arg Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln	
180 185 190	
caa gcg aaa gtg cac tgt gcg tat tgc gac ggc gcg tat gac caa atc	625
Gln Ala Lys Val His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile	
195 200 205	
ggc ttc ccc gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt	673
Gly Phe Pro Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe	
210 215 220	
cct tgg cac ccg ttc tac ctc tac tcc aac gag cgc ata ctc ggg aaa	721
Pro Trp His Arg Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys	
225 230 235 240	
ctt atc ggc gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg	769
Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala	
245 250 255	
ccg ggg ggc atg cag ttc ccg tct atc tac aca gac cct tca tcc tcg	817
Pro Gly Gly Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser	
260 265 270	
cta tat gac aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att	865
Leu Tyr Asp Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile	
275 280 285	
gac ctc gac tac aat ggc acc gat cct acc ttc tcc cct gaa gaa cag	913
Asp Leu Asp Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln	
290 295 300	

att aac cac aac ctc gcc gtc atg tac cga cag gtg ata tcc agt gga	961
Ile Asn His Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly	
305 310 315 320	
aag acg cca gag ctg ttt atg ggc tca gcg tac cgc gcc ggt gac cag	1009
Lys Thr Pro Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln	
325 330 335	
cct gac ccc ggc gca ggc tct gta gag cag aag ccg cac ggc ccg gtg	1057
Pro Asp Pro Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val	
340 345 350	
cat gtg tgg aca ggt gat cgc aac cag ccc aat cgc gaa gac atg ggc	1105
His Val Trp Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly	
355 360 365	
acg ctc tac tcg gcg gcg tgg gac ccc gtc ttc ttc gca cac cac ggc	1153
Thr Leu Tyr Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly	
370 375 380	
aac atc gac cgc atg tgg tac gtg tgg agg aac ctt ggc ggc aag cac	1201
Asn Ile Asp Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His	
385 390 395 400	
cgc aac ttc acc gac ccc gac tgg ctc aac gcg tcc ttc ctg ttc tat	1249
Arg Asn Phe Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr	
405 410 415	
gat gag aat gcg cag ctc gtc cgt gtt aaa gta aaa gac tgc tta gag	1297
Asp Glu Asn Ala Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu	
420 425 430	
gcc gac gca atg cgg tac aca tac cag gat gta gag atc ccg tgg ctc	1345
Ala Asp Ala Met Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu	
435 440 445	
aaa gca aag ccg acg cca aag agc gcc cta cag aag ata aag agc aag	1393
Lys Ala Lys Pro Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys	
450 455 460	
gta tcg acg ctg aag gca aca cca agg ggg acg acg act acc aca gca	1441
Val Ser Thr Leu Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Thr Ala	
465 470 475 480	
gag act aca ttt ccg gtg gtg ctg gat aag ccg gtg agt gca aca gtg	1489
Glu Thr Thr Phe Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val	

485	490	495	
gct aga ccg aag gcc agg agg agt ggg aag gag aag gaa gaa gag gag			1537
Ala Arg Pro Lys Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu Glu			
500	505	510	
gag gtg ttg gtg gtg gag gga atc gag ttg gag aag gac gtg ttc gtg			1585
Glu Val Leu Val Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val			
515	520	525	
aag ttt gat gtg tat ata aac tcg ccg gag cac gaa ggg gtg ggg ccg			1633
Lys Phe Asp Val Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro			
530	535	540	
gag gcg agt gag ttc gca ggg agc ttc gtc cac gtg cca cac aag cac			1681
Glu Ala Ser Glu Phe Ala Gly Ser Phe Val His Val Pro His Lys His			
545	550	555	560
aag aag gcg aag aag ggg aag gag atg gcc agg atg aac aca agg ctt			1729
Lys Lys Ala Lys Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu			
565	570	575	
aag ctc ggg ata acg gac ctg ctc gag gac atc ggc gct gag gac gac			1777
Lys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp			
580	585	590	
gag agc gtg ctc atc acg ctc gtg ccc agg agc ggc aag gga atg gtg			1825
Glu Ser Val Leu Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val			
595	600	605	
aag gtt gga ggg cta agg att gat ttc tcc aag tgatgagcat attgtgaaga			1878
Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys			
610	615		
gaaaatttgc atttaccgcc ctatagaatc gaaaatttgc gtatatgtcc cattattgtt			1938
ttttttattc ttcaagcgta ttcagaataa gagttgcgtg catgcacgca tgcagccatg			1998
ttgttgtagt cgatatgtgg ggtatgtttg gatcagggat aatgatgtga actttgaatt			2058
aattattaca ctctgagaat aaattagaga gtttattatg caagttgctt ggtgtaatag			2118
atattcaaca ttgtttccta tacatctttt ttggaagaa aaaaaaaaaa aaaaaaaatc			2178
gat			2181

<211> 619

<212> PRT

<213> pineapple.

<400> 20

Gly Ile Asp Lys Leu Asp Pro Val Pro Gly Leu Gly Val Phe Thr Met  
1 5 10 15

Ala Thr Leu Ser Lys Leu Ala Ser Gln Pro Ile Thr Pro Pro Leu Ser  
20 25 30

Pro Leu Pro Pro Leu His Ala Pro Ser Leu Thr Lys Ser Phe Thr Thr  
35 40 45

Thr Phe Leu Ser Pro Val Gly Val Pro Asn His Pro Val Ile Arg Ser  
50 55 60

His Ala Asn Leu Arg Ser Asn Lys Arg Met Pro Thr Ser Leu Arg Ala  
65 70 75 80

Ala Ser Pro Ala Ala Thr Tyr Ser Trp Ala Leu Gly Gly Leu Tyr Gly  
85 90 95

Ala Thr Thr Gly Leu Gly Leu Asn Arg Arg Ala Ala Ala Ala Pro Ile  
100 105 110

Leu Ala Pro Asp Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala  
115 120 125

Ser Ala Arg Pro Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile  
130 135 140

Asp Phe Lys Leu Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala  
145 150 155 160

Ala His Leu Val Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val  
165 170 175

Glu Leu Met Arg Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln  
180 185 190

Gln Ala Lys Val His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile  
195 200 205

Gly Phe Pro Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe  
210 215 220

Pro Trp His Arg Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys			
225	230	235	240
Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala			
	245	250	255
Pro Gly Gly Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser			
	260	265	270
Leu Tyr Asp Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile			
	275	280	285
Asp Leu Asp Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln			
	290	295	300
Ile Asn His Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly			
305	310	315	320
Lys Thr Pro Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln			
	325	330	335
Pro Asp Pro Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val			
	340	345	350
His Val Trp Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly			
	355	360	365
Thr Leu Tyr Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly			
	370	375	380
Asn Ile Asp Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His			
385	390	395	400
Arg Asn Phe Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr			
	405	410	415
Asp Glu Asn Ala Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu			
	420	425	430
Ala Asp Ala Met Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu			
	435	440	445
Lys Ala Lys Pro Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys			
	450	455	460
Val Ser Thr Leu Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Ala			
465	470	475	480

Glu Thr Thr Phe Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val  
485 490 495

Ala Arg Pro Lys Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu  
500 505 510

Glu Val Leu Val Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val  
515 520 525

Lys Phe Asp Val Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro  
530 535 540

Glu Ala Ser Glu Phe Ala Gly Ser Phe Val His Val Pro His Lys His  
545 550 555 560

Lys Lys Ala Lys Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu  
565 570 575

Lys Leu Gly Ile Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp  
580 585 590

Glu Ser Val Leu Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val  
595 600 605

Lys Val Gly Gly Leu Arg Ile Asp Phe Ser Lys  
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<210> 21

<211> 2078

<212> DNA

<213> banana

<220>

<221> CDS

<222> (53)..(1822)

<400> 21

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Met Ser

1

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Leu Leu Leu Asn Ser Ser Phe Thr Gly Ala Ser Ser Ala Cys Leu Leu

5

10

15

caa cgg gaa agg tcc cgc cgc cgc cgc ctc cac gtc cct ggc gtg aca	154
Gln Arg Glu Arg Ser Arg Arg Arg Arg Leu His Val Pro Gly Val Thr	
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tgC cgc cag ggc agt aat ggt gac cgc aga gat gcc gcc ccc cag cag	202
Cys Arg Gln Gly Ser Asn Gly Asp Arg Arg Asp Ala Ala Pro Gln Gln	
35 40 45 50	
cag tcg ccg ccg ctg ctg gat cgg cgc gac atg ctg ttg ggt tta gga	250
Gln Ser Pro Pro Leu Leu Asp Arg Arg Asp Met Leu Leu Gly Leu Gly	
55 60 65	
ggg ctt tac ggc gtg acc gca gga ccc aag gtt ctg gcg gcg ccg ata	298
Gly Leu Tyr Gly Val Thr Ala Gly Pro Lys Val Leu Ala Ala Pro Ile	
70 75 80	
atg ccg ccg gat ctg tcc aag tgc tac cct gcc acc gca cct gcc ctc	346
Met Pro Pro Asp Leu Ser Lys Cys Tyr Pro Ala Thr Ala Pro Ala Leu	
85 90 95	
gac aac aaa tgc tgc ccg cct tac gac ccc ggc gag acg atc tcg gag	394
Asp Asn Lys Cys Cys Pro Pro Tyr Asp Pro Gly Glu Thr Ile Ser Glu	
100 105 110	
tac agc ttc cct gct acg ccc ctc cgg gtg cgg cgg ccg gcc cat atc	442
Tyr Ser Phe Pro Ala Thr Pro Leu Arg Val Arg Arg Pro Ala His Ile	
115 120 125 130	
gtg aag gac gat cag gag tat atg gac aag tac aag gag gca gtg agg	490
Val Lys Asp Asp Gln Glu Tyr Met Asp Lys Tyr Lys Glu Ala Val Arg	
135 140 145	
agg atg aag aat ctg ccg gca gac cac cct tgg aac tac tac cag cag	538
Arg Met Lys Asn Leu Pro Ala Asp His Pro Trp Asn Tyr Tyr Gln Gln	
150 155 160	
gcg aac atc cac tgc cag tat tgc aac tac gcc tac cac cag caa aat	586
Ala Asn Ile His Cys Gln Tyr Cys Asn Tyr Ala Tyr His Gln Gln Asn	
165 170 175	
acc gac gac gtg ccc atc cag gtc cac ttc agc tgg atc ttc ctc cca	634
Thr Asp Asp Val Pro Ile Gln Val His Phe Ser Trp Ile Phe Leu Pro	
180 185 190	
tgg cac cgc tac tac ctc cac ttc tac gaa agg atc ctc ggc aag ctc	682
Trp His Arg Tyr Tyr Leu His Phe Tyr Glu Arg Ile Leu Gly Lys Leu	
195 200 205 210	



atc gac gac gac acc ttc acc atc cca ttc tgg aac tgg gac acc aag	730
Ile Asp Asp Asp Thr Phe Thr Ile Pro Phe Trp Asn Trp Asp Thr Lys	
215 220 225	
gac ggg atg acg ttc ccc gcc atc ttc cag gat gcg gca tcc ccg ctg	778
Asp Gly Met Thr Phe Pro Ala Ile Phe Gln Asp Ala Ala Ser Pro Leu	
230 235 240	
tac gac ccg aga cgc gac caa cgc cac gtc aag gac ggc aag atc ctc	826
Tyr Asp Pro Arg Arg Asp Gln Arg His Val Lys Asp Gly Lys Ile Leu	
245 250 255	
gac ctc aag tac gcc tac acc gaa aac act gca tcc gac agc gag atc	874
Asp Leu Lys Tyr Ala Tyr Thr Glu Asn Thr Ala Ser Asp Ser Glu Ile	
260 265 270	
ata cgg gag aac ctc tgc ttc ata cag aag acg ttc aag cac agc ctg	922
Ile Arg Glu Asn Leu Cys Phe Ile Gln Lys Thr Phe Lys His Ser Leu	
275 280 285 290	
tcg ctg gcg gaa ctg ttc atg ggg gat ccc gtg cgc gcg ggg gag aag	970
Ser Leu Ala Glu Leu Phe Met Gly Asp Pro Val Arg Ala Gly Glu Lys	
295 300 305	
gag atc cag gag gct aat ggg cag atg gaa gtc atc cac aat gcg gcg	1018
Glu Ile Gln Glu Ala Asn Gly Gln Met Glu Val Ile His Asn Ala Ala	
310 315 320	
cac atg tgg gtc gga gag ccg gac gga tac aag gaa aac atg ggg gac	1066
His Met Trp Val Gly Glu Pro Asp Gly Tyr Lys Glu Asn Met Gly Asp	
325 330 335	
ttc tcc acc gcc gcc cgc gat tct gtt ttc ttc tgc cac cat tcc aat	1114
Phe Ser Thr Ala Ala Arg Asp Ser Val Phe Phe Cys His His Ser Asn	
340 345 350	
gtc gac cgc atg tgg gac atc tac cgc aac ctc cgc ggc aac cgc gtc	1162
Val Asp Arg Met Trp Asp Ile Tyr Arg Asn Leu Arg Gly Asn Arg Val	
355 360 365 370	
gag ttc gaa gac aac gac tgg ttg gac agc acc ttc ctc ttc cac gac	1210
Glu Phe Glu Asp Asn Asp Trp Leu Asp Ser Thr Phe Leu Phe His Asp	
375 380 385	
gag aac gaa cag ctc gtc aaa gtc aag atg agc gac tgc ctc aac ccg	1258
Glu Asn Glu Gln Leu Val Lys Val Lys Met Ser Asp Cys Leu Asn Pro	
390 395 400	

acc aag ctt cgg tac acg ttc gag caa gtt ccc ctc cca tgg ctg ggc	1306
Thr Lys Leu Arg Tyr Thr Phe Glu Gln Val Pro Leu Pro Trp Leu Gly	
405 410 415	
aaa atc aat tgc cag aag acg gca gag acg aag tcc aag gcc acg acg	1354
Lys Ile Asn Cys Gln Lys Thr Ala Glu Thr Lys Ser Lys Ala Thr Thr	
420 425 430	
gag ctg tcg ctg acg cgc gtg aac gaa ttc ggg acg acg gcc cag gca	1402
Glu Leu Ser Leu Thr Arg Val Asn Glu Phe Gly Thr Thr Ala Gln Ala	
435 440 445 450	
ctc gac gcg agc aac ccg ctg cgg gtg atc gtg gca agg ccg aag aag	1450
Leu Asp Ala Ser Asn Pro Leu Arg Val Ile Val Ala Arg Pro Lys Lys	
455 460 465	
aac cgc aag aag aag gag aag caa gag aag gtg ggg gtg att cag atc	1498
Asn Arg Lys Lys Lys Glu Lys Gln Glu Lys Val Gly Val Ile Gln Ile	
470 475 480	
aag gat att aag gtg acc acc aac gag aca gct cgc ttc gac gtc tat	1546
Lys Asp Ile Lys Val Thr Thr Asn Glu Thr Ala Arg Phe Asp Val Tyr	
485 490 495	
gtc gcg gtt cct tac ggt gac ctc gcc gga ccc gac tac ggc gag ttc	1594
Val Ala Val Pro Tyr Gly Asp Leu Ala Gly Pro Asp Tyr Gly Glu Phe	
500 505 510	
gcg ggc agc tac gtg agg ctg gcg cat agg atg aag gga agc gac ggg	1642
Ala Gly Ser Tyr Val Arg Leu Ala His Arg Met Lys Gly Ser Asp Gly	
515 520 525 530	
acc gaa aag cag ggc ccc aag aag aag gga aaa ctc aag ctg ggt att	1690
Thr Glu Lys Gln Gly Pro Lys Lys Lys Gly Lys Leu Lys Leu Gly Ile	
535 540 545	
acg ccg ctg ctc gag gac atc gat gct gag gac gcc gac aag ttg gtg	1738
Thr Pro Leu Leu Glu Asp Ile Asp Ala Glu Asp Ala Asp Lys Leu Val	
550 555 560	
gtc acc ctg gtt ctc cgc act ggg agc gtc acc gtg ggg gga gtt tcc	1786
Val Thr Leu Val Leu Arg Thr Gly Ser Val Thr Val Gly Gly Val Ser	
565 570 575	
atc aat ctc ctg cag aca gat tct acc gcc gcc atc taaatgatgg	1832
Ile Asn Leu Leu Gln Thr Asp Ser Thr Ala Ala Ile	
580 585 590	

cctcggatca cagcttctcc ccgcttaagt tggagtgatc gattactggg gctgctttct 1892  
 tcctccctgt cggttcttgct atcttcttga tctggaacga tccttcaata attagggcat 1952  
 gacagtagtc gtcgcccgat cccatatgta cgtgttggtc tcaacagctg tacatgtgac 2012  
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 aaaaaa 2078

<210> 22  
 <211> 590  
 <212> PRT  
 <213> banana

<400> 22

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			20					25					30		
Val	Thr	Cys	Arg	Gln	Gly	Ser	Asn	Gly	Asp	Arg	Arg	Asp	Ala	Ala	Pro
		35					40					45			
Gln	Gln	Gln	Ser	Pro	Pro	Leu	Leu	Asp	Arg	Arg	Asp	Met	Leu	Leu	Gly
		50					55					60			
Leu	Gly	Gly	Leu	Tyr	Gly	Val	Thr	Ala	Gly	Pro	Lys	Val	Leu	Ala	Ala
	65				70				75					80	
Pro	Ile	Met	Pro	Pro	Asp	Leu	Ser	Lys	Cys	Tyr	Pro	Ala	Thr	Ala	Pro
					85				90					95	
Ala	Leu	Asp	Asn	Lys	Cys	Cys	Pro	Pro	Tyr	Asp	Pro	Gly	Glu	Thr	Ile
			100						105				110		
Ser	Glu	Tyr	Ser	Phe	Pro	Ala	Thr	Pro	Leu	Arg	Val	Arg	Arg	Pro	Ala
		115					120					125			
His	Ile	Val	Lys	Asp	Asp	Gln	Glu	Tyr	Met	Asp	Lys	Tyr	Lys	Glu	Ala
		130					135					140			
Val	Arg	Arg	Met	Lys	Asn	Leu	Pro	Ala	Asp	His	Pro	Trp	Asn	Tyr	Tyr
	145					150					155			160	

Gln	Gln	Ala	Asn	Ile	His	Cys	Gln	Tyr	Cys	Asn	Tyr	Ala	Tyr	His	Gln	165	170	175	
Gln	Asn	Thr	Asp	Asp	Val	Pro	Ile	Gln	Val	His	Phe	Ser	Trp	Ile	Phe	180	185	190	
Leu	Pro	Trp	His	Arg	Tyr	Tyr	Leu	His	Phe	Tyr	Glu	Arg	Ile	Leu	Gly	195	200	205	
Lys	Leu	Ile	Asp	Asp	Asp	Thr	Phe	Thr	Ile	Pro	Phe	Trp	Asn	Trp	Asp	210	215	220	
Thr	Lys	Asp	Gly	Met	Thr	Phe	Pro	Ala	Ile	Phe	Gln	Asp	Ala	Ala	Ser	225	230	235	240
Pro	Leu	Tyr	Asp	Pro	Arg	Arg	Asp	Gln	Arg	His	Val	Lys	Asp	Gly	Lys	245	250	255	
Ile	Leu	Asp	Leu	Lys	Tyr	Ala	Tyr	Thr	Glu	Asn	Thr	Ala	Ser	Asp	Ser	260	265	270	
Glu	Ile	Ile	Arg	Glu	Asn	Leu	Cys	Phe	Ile	Gln	Lys	Thr	Phe	Lys	His	275	280	285	
Ser	Leu	Ser	Leu	Ala	Glu	Leu	Phe	Met	Gly	Asp	Pro	Val	Arg	Ala	Gly	290	295	300	
Glu	Lys	Glu	Ile	Gln	Glu	Ala	Asn	Gly	Gln	Met	Glu	Val	Ile	His	Asn	305	310	315	320
Ala	Ala	His	Met	Trp	Val	Gly	Glu	Pro	Asp	Gly	Tyr	Lys	Glu	Asn	Met	325	330	335	
Gly	Asp	Phe	Ser	Thr	Ala	Ala	Arg	Asp	Ser	Val	Phe	Phe	Cys	His	His	340	345	350	
Ser	Asn	Val	Asp	Arg	Met	Trp	Asp	Ile	Tyr	Arg	Asn	Leu	Arg	Gly	Asn	355	360	365	
Arg	Val	Glu	Phe	Glu	Asp	Asn	Asp	Trp	Leu	Asp	Ser	Thr	Phe	Leu	Phe	370	375	380	
His	Asp	Glu	Asn	Glu	Gln	Leu	Val	Lys	Val	Lys	Met	Ser	Asp	Cys	Leu	385	390	395	400
Asn	Pro	Thr	Lys	Leu	Arg	Tyr	Thr	Phe	Glu	Gln	Val	Pro	Leu	Pro	Trp	405	410	415	

Leu Gly Lys Ile Asn Cys Gln Lys Thr Ala Glu Thr Lys Ser Lys Ala  
 420 425 430

Thr Thr Glu Leu Ser Leu Thr Arg Val Asn Glu Phe Gly Thr Thr Ala  
 435 440 445

Gln Ala Leu Asp Ala Ser Asn Pro Leu Arg Val Ile Val Ala Arg Pro  
 450 455 460

Lys Lys Asn Arg Lys Lys Lys Glu Lys Gln Glu Lys Val Gly Val Ile  
 465 470 475 480

Gln Ile Lys Asp Ile Lys Val Thr Thr Asn Glu Thr Ala Arg Phe Asp  
 485 490 495

Val Tyr Val Ala Val Pro Tyr Gly Asp Leu Ala Gly Pro Asp Tyr Gly  
 500 505 510

Glu Phe Ala Gly Ser Tyr Val Arg Leu Ala His Arg Met Lys Gly Ser  
 515 520 525

Asp Gly Thr Glu Lys Gln Gly Pro Lys Lys Lys Gly Lys Leu Lys Leu  
 530 535 540

Gly Ile Thr Pro Leu Leu Glu Asp Ile Asp Ala Glu Asp Ala Asp Lys  
 545 550 555 560

Leu Val Val Thr Leu Val Leu Arg Thr Gly Ser Val Thr Val Gly Gly  
 565 570 575

Val Ser Ile Asn Leu Leu Gln Thr Asp Ser Thr Ala Ala Ile  
 580 585 590

<210> 23

<211> 900

<212> DNA

<213> banana

<220>

<221> CDS

<222> (13)..(729)

<400> 23

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gag ttc gtc gac cag gag tgg ctc gag tct gaa ttc acc ttc tac gac				99
Glu Phe Val Asp Gln Glu Trp Leu Glu Ser Glu Phe Thr Phe Tyr Asp				
15	20	25		
gag aat gtg cgc ctg cgc agg atc aag gtg cgc gac gtg ttg aac ata				147
Glu Asn Val Arg Leu Arg Arg Ile Lys Val Arg Asp Val Leu Asn Ile				
30	35	40	45	
gac aaa ctc agg tac cgg tac gaa gac atc gac atg cca tgg ctc gct				195
Asp Lys Leu Arg Tyr Arg Tyr Glu Asp Ile Asp Met Pro Trp Leu Ala				
50	55	60		
gca cgt ccc aag cct tcc gtt cac cct aag atc gcg cgc gac ata ttg				243
Ala Arg Pro Lys Pro Ser Val His Pro Lys Ile Ala Arg Asp Ile Leu				
65	70	75		
aag aag cgt aat ggc gaa ggc gta ctg aga atg ccc ggc gaa acg gat				291
Lys Lys Arg Asn Gly Glu Gly Val Leu Arg Met Pro Gly Glu Thr Asp				
80	85	90		
cgt tca caa ctc tcc gaa gat ggt agc tgg aca ctg gac aag agc atc				339
Arg Ser Gln Leu Ser Glu Asp Gly Ser Trp Thr Leu Asp Lys Ser Ile				
95	100	105		
acc gtg agg gtt gac agg cca agg atc aac agg aca ggg caa gaa aaa				387
Thr Val Arg Val Asp Arg Pro Arg Ile Asn Arg Thr Gly Gln Glu Lys				
110	115	120	125	
gag gaa gaa gag gag atc tta ttg gtc tac gga atc gat act aag aga				435
Glu Glu Glu Glu Glu Ile Leu Leu Val Tyr Gly Ile Asp Thr Lys Arg				
130	135	140		
agc aga ttc gtc aaa ttc gat gtg ttc atc aac gtc gtc gac gaa acc				483
Ser Arg Phe Val Lys Phe Asp Val Phe Ile Asn Val Val Asp Glu Thr				
145	150	155		
gtg ctg aac cca aag tcg agg gag ttc gca ggg acc ttc gtc aat ctc				531
Val Leu Asn Pro Lys Ser Arg Glu Phe Ala Gly Thr Phe Val Asn Leu				
160	165	170		
cac cac gtc tcg agg acg aaa agc cat gag gat ggc ggc gtg ggt tcg				579
His His Val Ser Arg Thr Lys Ser His Glu Asp Gly Gly Val Gly Ser				
175	180	185		
aag atg aaa agc cac ctt aag ctc ggt ata tcg gaa ctt ttg gaa gac				627
Lys Met Lys Ser His Leu Lys Leu Gly Ile Ser Glu Leu Leu Glu Asp				

190	195	200	205	
ctc gag gca gac gaa gat gat tgc atc tgg gtg aca ctg gtg cca aga				675
Leu Glu Ala Asp Glu Asp Asp Cys Ile Trp Val Thr Leu Val Pro Arg				
210	215	220		
ggc ggc acg ggg gtc aac acc acc gta gac ggc gtc cgg atc gac tac				723
Gly Gly Thr Gly Val Asn Thr Thr Val Asp Gly Val Arg Ile Asp Tyr				
225	230	235		
atg aag tagtgaaccg gcacgccgct cctcccctcc ccatcagaag tgggtataata				779
Met Lys				
tttatattgg atcgaggctc gtggtatctt ttgataagag taagttccat aaatttagaa				839
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<210> 24
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<212> PRT
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<400> 24

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			20					25					30		
Arg	Leu	Arg	Arg	Ile	Lys	Val	Arg	Asp	Val	Leu	Asn	Ile	Asp	Lys	Leu
		35					40					45			
Arg	Tyr	Arg	Tyr	Glu	Asp	Ile	Asp	Met	Pro	Trp	Leu	Ala	Ala	Arg	Pro
	50					55					60				
Lys	Pro	Ser	Val	His	Pro	Lys	Ile	Ala	Arg	Asp	Ile	Leu	Lys	Lys	Arg
65					70					75					80
Asn	Gly	Glu	Gly	Val	Leu	Arg	Met	Pro	Gly	Glu	Thr	Asp	Arg	Ser	Gln
				85					90					95	
Leu	Ser	Glu	Asp	Gly	Ser	Trp	Thr	Leu	Asp	Lys	Ser	Ile	Thr	Val	Arg
			100					105						110	

Val Asp Arg Pro Arg Ile Asn Arg Thr Gly Gln Glu Lys Glu Glu Glu  
115 120 125

Glu Glu Ile Leu Leu Val Tyr Gly Ile Asp Thr Lys Arg Ser Arg Phe  
130 135 140

Val Lys Phe Asp Val Phe Ile Asn Val Val Asp Glu Thr Val Leu Asn  
145 150 155 160

Pro Lys Ser Arg Glu Phe Ala Gly Thr Phe Val Asn Leu His His Val  
165 170 175

Ser Arg Thr Lys Ser His Glu Asp Gly Gly Val Gly Ser Lys Met Lys  
180 185 190

Ser His Leu Lys Leu Gly Ile Ser Glu Leu Leu Glu Asp Leu Glu Ala  
195 200 205

Asp Glu Asp Asp Cys Ile Trp Val Thr Leu Val Pro Arg Gly Gly Thr  
210 215 220

Gly Val Asn Thr Thr Val Asp Gly Val Arg Ile Asp Tyr Met Lys  
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<210> 25

<211> 1522

<212> DNA

<213> pineapple

<220>

<221> CDS

<222> (3)..(1271)

<400> 25

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gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt cct tgg cac 95  
Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His  
20 25 30

cgg ttc tac ctc tac tcc aac gag cgc ata ctc ggc aaa ctt atc ggc 143  
Arg Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly  
35 40 45

gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg ccg ggg ggc 191



Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly	
50 55 60	
atg cag ttc ccg tct atc tac acg gac cct tca tcc tcg cta tat gac	239
Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp	
65 70 75	
aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att gac ctc gac	287
Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp	
80 85 90 95	
tac aat ggc acc gat cct acc ttc tcc cct gaa gaa cag att aac cac	335
Tyr Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His	
100 105 110	
aac ctc gcc gtc atg tac cga cag gtg ata tcc agt gga aag aca cca	383
Asn Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro	
115 120 125	
gag ctg ttt atg ggc tca gcg tac cgc gcc ggt gac cag cct gac ccc	431
Glu Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro	
130 135 140	
ggc gca ggc tct gta gag cag aag ccg cac ggc ccg gtg cat gtg tgg	479
Gly Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp	
145 150 155	
aca ggt gat cgc aac cag ccc aat cgc gaa gac atg ggc acg ctc tac	527
Thr Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr	
160 165 170 175	
tcg gcg gcg tgg gac ccc gtc ttc ttc gca cac cac ggc aac atc gac	575
Ser Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp	
180 185 190	
cgc atg tgg tac gtg tgg agg aac ctt ggc ggc aag cac cgc aac ttc	623
Arg Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe	
195 200 205	
acc gac ccc gac tgg ctc aac gcg tcc ttc ctg ttc tat gat gag aat	671
Thr Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn	
210 215 220	
gcg cag ctc gtc cgt gtt aaa gta aaa gac tgc tta gag gcc gac gca	719
Ala Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu Ala Asp Ala	
225 230 235	

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atttaccgcc ctatagaatc gaaaaattgc gtatatgtcc cattattggt ttttttattc 1361  
 ttcaagcgta ttcagaataa gagttgcgtg catgcacgca tgcagccatg ttgttgtagt 1421  
 cgatatgtgg ggtatgtttg gatcagggat aatgatgtga actttgaatt aattattaca 1481  
 ctctgagaat aaattagaga gtttattatg caaaaaaaaa a 1522

<210> 26  
 <211> 423  
 <212> PRT  
 <213> pineapple

<400> 26  
 His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro Asp  
 1 5 10 15  
 Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His Arg  
 20 25 30  
 Phe Tyr Leu Tyr Ser Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp  
 35 40 45  
 Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly Met  
 50 55 60  
 Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp Lys  
 65 70 75 80  
 Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp Tyr  
 85 90 95  
 Asn Gly Thr Asp Pro Thr Phe Ser Pro Glu Glu Gln Ile Asn His Asn  
 100 105 110  
 Leu Ala Val Met Tyr Arg Gln Val Ile Ser Ser Gly Lys Thr Pro Glu  
 115 120 125  
 Leu Phe Met Gly Ser Ala Tyr Arg Ala Gly Asp Gln Pro Asp Pro Gly  
 130 135 140  
 Ala Gly Ser Val Glu Gln Lys Pro His Gly Pro Val His Val Trp Thr  
 145 150 155 160  
 Gly Asp Arg Asn Gln Pro Asn Arg Glu Asp Met Gly Thr Leu Tyr Ser  
 165 170 175

Ala Ala Trp Asp Pro Val Phe Phe Ala His His Gly Asn Ile Asp Arg  
180 185 190

Met Trp Tyr Val Trp Arg Asn Leu Gly Gly Lys His Arg Asn Phe Thr  
195 200 205

Asp Pro Asp Trp Leu Asn Ala Ser Phe Leu Phe Tyr Asp Glu Asn Ala  
210 215 220

Gln Leu Val Arg Val Lys Val Lys Asp Cys Leu Glu Ala Asp Ala Met  
225 230 235 240

Arg Tyr Thr Tyr Gln Asp Val Glu Ile Pro Trp Leu Lys Ala Lys Pro  
245 250 255

Thr Pro Lys Ser Ala Leu Gln Lys Ile Lys Ser Lys Val Ser Thr Leu  
260 265 270

Lys Ala Thr Pro Arg Gly Thr Thr Thr Thr Thr Ala Glu Thr Thr Phe  
275 280 285

Pro Val Val Leu Asp Lys Pro Val Ser Ala Thr Val Ala Arg Pro Lys  
290 295 300

Ala Arg Arg Ser Gly Lys Glu Lys Glu Glu Glu Glu Glu Val Leu Val  
305 310 315 320

Val Glu Gly Ile Glu Leu Glu Lys Asp Val Phe Val Lys Phe Asp Val  
325 330 335

Tyr Ile Asn Ser Pro Glu His Glu Gly Val Gly Pro Glu Ala Ser Glu  
340 345 350

Phe Ala Gly Ser Phe Val His Val Pro His Lys His Lys Lys Ala Lys  
355 360 365

Lys Gly Lys Glu Met Ala Arg Met Asn Thr Arg Leu Lys Leu Gly Ile  
370 375 380

Thr Asp Leu Leu Glu Asp Ile Gly Ala Glu Asp Asp Glu Ser Val Leu  
385 390 395 400

Ile Thr Leu Val Pro Arg Ser Gly Lys Gly Met Val Lys Val Gly Gly  
405 410 415

Leu Arg Ile Asp Phe Ser Lys  
420

<210> 27  
 <211> 875  
 <212> DNA  
 <213> pineapple

<220>  
 <221> CDS  
 <222> (3)..(875)

<400> 27  
 ac aac aaa cca gtg cct ggt tta ggt gta ttc act atg gcc acc ctc 47  
 Asn Lys Pro Val Pro Gly Leu Gly Val Phe Thr Met Ala Thr Leu  
 1 5 10 15  
 tct aaa cta gct tcc cca acc aat aac acc tcc act ctc ccc gct ccc 95  
 Ser Lys Leu Ala Ser Pro Thr Asn Asn Thr Ser Thr Leu Pro Ala Pro  
 20 25 30  
 tcc ttt gca tgc tcc ttc tct cac caa aag ctt cac cac cac ctt cct 143  
 Ser Phe Ala Cys Ser Phe Ser His Gln Lys Leu His His His Leu Pro  
 35 40 45  
 ctc ccc tgt agg ggt ccc aaa cca ccc cgt cat aag atc tca tgc aaa 191  
 Leu Pro Cys Arg Gly Pro Lys Pro Pro Arg His Lys Ile Ser Cys Lys  
 50 55 60  
 tct aag gag caa caa gag aat gcc gac aag cct gcg ggc cgc atc gac 239  
 Ser Lys Glu Gln Gln Glu Asn Ala Asp Lys Pro Ala Gly Arg Ile Asp  
 65 70 75  
 cgc cgc gac cta ctc ctg ggc ctc ggc ggg ctt tac ggt gcc acc act 287  
 Arg Arg Asp Leu Leu Leu Gly Leu Gly Gly Leu Tyr Gly Ala Thr Thr  
 80 85 90 95  
 ggg ctc ggc ctc aac cgt cga gcg gcc gcc gcc cct atc ctg gct ccc 335  
 Gly Leu Gly Leu Asn Arg Arg Ala Ala Ala Ala Pro Ile Leu Ala Pro  
 100 105 110  
 gac ctc tca act tgt ggg ccg cct gcc gac ctc cct gcc tcc gcc cga 383  
 Asp Leu Ser Thr Cys Gly Pro Pro Ala Asp Leu Pro Ala Ser Ala Arg  
 115 120 125  
 ccg aca gtt tgc tgc ccg cca tac caa tcc acc atc atc gtc ttc aag 431  
 Pro Thr Val Cys Cys Pro Pro Tyr Gln Ser Thr Ile Ile Val Phe Lys  
 130 135 140

ctc ccc ccg cga tct gct ccg ctt cgc gtc cgg cct gcg gcc cac ttg	479
Leu Pro Pro Arg Ser Ala Pro Leu Arg Val Arg Pro Ala Ala His Leu	
145 150 155	
gtt gac gcc gac tac ctg gcc aag tat aag aag gcg gtc gag ctc atg	527
Val Asp Ala Asp Tyr Leu Ala Lys Tyr Lys Lys Ala Val Glu Leu Met	
160 165 170 175	
agg gcc ctg ccg gcc gac gac ccg cgc aac ttc gta cag caa gcg aaa	575
Arg Ala Leu Pro Ala Asp Asp Pro Arg Asn Phe Val Gln Gln Ala Lys	
180 185 190	
gtg cac tgt gcg tac tgc gac ggc gcg tac gac caa atc ggc ttc ccc	623
Val His Cys Ala Tyr Cys Asp Gly Ala Tyr Asp Gln Ile Gly Phe Pro	
195 200 205	
gat ctc gag atc cag atc cac aac tcg tgg ctc ttc ttt cct tgg cac	671
Asp Leu Glu Ile Gln Ile His Asn Ser Trp Leu Phe Phe Pro Trp His	
210 215 220	
cgg ttc tac ctc tac ttc aac gag cgc ata ctc ggg aaa ctt atc ggt	719
Arg Phe Tyr Leu Tyr Phe Asn Glu Arg Ile Leu Gly Lys Leu Ile Gly	
225 230 235	
gac gac acg ttc gcg ctg cct ttc tgg aac tgg gac gcg ccg ggg ggc	767
Asp Asp Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Gly Gly	
240 245 250 255	
atg cag ttc ccg tct atc tac aca gac cct tca tcc tcg cta tat gac	815
Met Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp	
260 265 270	
aag ctg cgt gat gcg aag cac cag ccg ccg act ttg att gac ctc gac	863
Lys Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp	
275 280 285	
tac aat ggc aca	875
Tyr Asn Gly Thr	
290	

<210> 28

<211> 291

<212> PRT

<213> pineapple

<400> 28

Asn	Lys	Pro	Val	Pro	Gly	Leu	Gly	Val	Phe	Thr	Met	Ala	Thr	Leu	Ser	1	5	10	15
Lys	Leu	Ala	Ser	Pro	Thr	Asn	Asn	Thr	Ser	Thr	Leu	Pro	Ala	Pro	Ser	20	25	30	
Phe	Ala	Cys	Ser	Phe	Ser	His	Gln	Lys	Leu	His	His	His	Leu	Pro	Leu	35	40	45	
Pro	Cys	Arg	Gly	Pro	Lys	Pro	Pro	Arg	His	Lys	Ile	Ser	Cys	Lys	Ser	50	55	60	
Lys	Glu	Gln	Gln	Glu	Asn	Ala	Asp	Lys	Pro	Ala	Gly	Arg	Ile	Asp	Arg	65	70	75	80
Arg	Asp	Leu	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Tyr	Gly	Ala	Thr	Thr	Gly	85	90	95	
Leu	Gly	Leu	Asn	Arg	Arg	Ala	Ala	Ala	Ala	Pro	Ile	Leu	Ala	Pro	Asp	100	105	110	
Leu	Ser	Thr	Cys	Gly	Pro	Pro	Ala	Asp	Leu	Pro	Ala	Ser	Ala	Arg	Pro	115	120	125	
Thr	Val	Cys	Cys	Pro	Pro	Tyr	Gln	Ser	Thr	Ile	Ile	Val	Phe	Lys	Leu	130	135	140	
Pro	Pro	Arg	Ser	Ala	Pro	Leu	Arg	Val	Arg	Pro	Ala	Ala	His	Leu	Val	145	150	155	160
Asp	Ala	Asp	Tyr	Leu	Ala	Lys	Tyr	Lys	Lys	Ala	Val	Glu	Leu	Met	Arg	165	170	175	
Ala	Leu	Pro	Ala	Asp	Asp	Pro	Arg	Asn	Phe	Val	Gln	Gln	Ala	Lys	Val	180	185	190	
His	Cys	Ala	Tyr	Cys	Asp	Gly	Ala	Tyr	Asp	Gln	Ile	Gly	Phe	Pro	Asp	195	200	205	
Leu	Glu	Ile	Gln	Ile	His	Asn	Ser	Trp	Leu	Phe	Phe	Pro	Trp	His	Arg	210	215	220	
Phe	Tyr	Leu	Tyr	Phe	Asn	Glu	Arg	Ile	Leu	Gly	Lys	Leu	Ile	Gly	Asp	225	230	235	240
Asp	Thr	Phe	Ala	Leu	Pro	Phe	Trp	Asn	Trp	Asp	Ala	Pro	Gly	Gly	Met	245	250	255	

Gln Phe Pro Ser Ile Tyr Thr Asp Pro Ser Ser Ser Leu Tyr Asp Lys  
 260 265 270

Leu Arg Asp Ala Lys His Gln Pro Pro Thr Leu Ile Asp Leu Asp Tyr  
 275 280 285

Asn Gly Thr  
 290

<210> 29  
 <211> 2057  
 <212> DNA  
 <213> lettuce

<220>  
 <221> CDS  
 <222> (16)..(1842)

<400> 29  
 gaccacccat agatg atg gct tct ctc gcc ttg tct agt ctt ccc acc tcc 51  
 Met Ala Ser Leu Ala Leu Ser Ser Leu Pro Thr Ser  
 1 5 10  
 acc aca acc aaa aaa ccc tta ttt tcc aaa aca tcc tcg cat gtt aag 99  
 Thr Thr Thr Lys Lys Pro Leu Phe Ser Lys Thr Ser Ser His Val Lys  
 15 20 25  
 cca ttc cat cgc ttc aaa gtt tca tgc aat gca ccc gct gat aac aat 147  
 Pro Phe His Arg Phe Lys Val Ser Cys Asn Ala Pro Ala Asp Asn Asn  
 30 35 40  
 gac aaa acc gtc aat aat tct gat acc cca aag ctc ata cta ccc aaa 195  
 Asp Lys Thr Val Asn Asn Ser Asp Thr Pro Lys Leu Ile Leu Pro Lys  
 45 50 55 60  
 aca cca ctt gaa acg cag aac gta gac agg aga aac ttg ctt ctg gga 243  
 Thr Pro Leu Glu Thr Gln Asn Val Asp Arg Arg Asn Leu Leu Leu Gly  
 65 70 75  
 ctc gga ggt ctc tac ggc gct gcc aac ttg acg acc att ccg tca gcc 291  
 Leu Gly Gly Leu Tyr Gly Ala Ala Asn Leu Thr Thr Ile Pro Ser Ala  
 80 85 90  
 ttt ggc att ccc atc gct gct cca gac aat att tca gac tgt gtt gct 339  
 Phe Gly Ile Pro Ile Ala Ala Pro Asp Asn Ile Ser Asp Cys Val Ala  
 95 100 105



gcg act tca aac cta agg aac agc aaa gac gct ata agg gga cta gcg	387
Ala Thr Ser Asn Leu Arg Asn Ser Lys Asp Ala Ile Arg Gly Leu Ala	
110 115 120	
tgt tgt cct ccg gtg ctt tca aca aac aaa cca atg gat tac gtc ctt	435
Cys Cys Pro Pro Val Leu Ser Thr Asn Lys Pro Met Asp Tyr Val Leu	
125 130 135 140	
cct tca aac cct gtg att cgt gtt cga cca gct gca cag aaa gcc act	483
Pro Ser Asn Pro Val Ile Arg Val Arg Pro Ala Ala Gln Lys Ala Thr	
145 150 155	
gcc gat tac act gct aag tat caa caa gca att caa gcc atg aag gat	531
Ala Asp Tyr Thr Ala Lys Tyr Gln Gln Ala Ile Gln Ala Met Lys Asp	
160 165 170	
ctc ccc gag gac cac cca cat agc tgg aag caa caa ggc aag att cac	579
Leu Pro Glu Asp His Pro His Ser Trp Lys Gln Gln Gly Lys Ile His	
175 180 185	
tgt gct tat tgc aac ggt ggt tac aat caa gaa caa agt ggt tac ccg	627
Cys Ala Tyr Cys Asn Gly Gly Tyr Asn Gln Glu Gln Ser Gly Tyr Pro	
190 195 200	
aat tta caa ctt cag att cac aac tca tgg ctc ttc ttt cct ttc cac	675
Asn Leu Gln Leu Gln Ile His Asn Ser Trp Leu Phe Phe Pro Phe His	
205 210 215 220	
cgg tgg tac ctc tat ttc tac gag aag ata ttg ggg aag ttg att aat	723
Arg Trp Tyr Leu Tyr Phe Tyr Glu Lys Ile Leu Gly Lys Leu Ile Asn	
225 230 235	
gat cca act ttc gct cta cct tac tgg aac tgg gat aac cct act gga	771
Asp Pro Thr Phe Ala Leu Pro Tyr Trp Asn Trp Asp Asn Pro Thr Gly	
240 245 250	
atg gtt att cct gcc atg ttc gaa cag aac agc aaa act aac tct ctg	819
Met Val Ile Pro Ala Met Phe Glu Gln Asn Ser Lys Thr Asn Ser Leu	
255 260 265	
ttt gac cct tta agg gat gcg aaa cac ctc cca cct tct atc ttt gat	867
Phe Asp Pro Leu Arg Asp Ala Lys His Leu Pro Pro Ser Ile Phe Asp	
270 275 280	
gtt gaa tat gct ggt gca gac act ggt gcc act tgt ata gac cag ata	915
Val Glu Tyr Ala Gly Ala Asp Thr Gly Ala Thr Cys Ile Asp Gln Ile	

285	290	295	300	
gcc att aat ctg tct tca atg tac aga cag atg gtc acc aac tcc act				963
Ala Ile Asn Leu Ser Ser Met Tyr Arg Gln Met Val Thr Asn Ser Thr				
	305	310	315	
gat aca aaa cga ttc ttc ggt ggc gaa ttt gta gct gga aat gac cct				1011
Asp Thr Lys Arg Phe Phe Gly Gly Glu Phe Val Ala Gly Asn Asp Pro				
	320	325	330	
ctt gcg agc gag ttc aac gta gct ggg acc gta gaa gct ggg gtt cac				1059
Leu Ala Ser Glu Phe Asn Val Ala Gly Thr Val Glu Ala Gly Val His				
	335	340	345	
act gcg gct cac cgc tgg gtg ggt aat tct agg atg gcc aac agc gaa				1107
Thr Ala Ala His Arg Trp Val Gly Asn Ser Arg Met Ala Asn Ser Glu				
	350	355	360	
gac atg ggg aac ttc tac tcc gca gga tat gat cct ctc ttt tac gtc				1155
Asp Met Gly Asn Phe Tyr Ser Ala Gly Tyr Asp Pro Leu Phe Tyr Val				
	365	370	380	
cac cat gcg aat gtc gac agg atg tgg caa atc tgg aaa gat att gac				1203
His His Ala Asn Val Asp Arg Met Trp Gln Ile Trp Lys Asp Ile Asp				
	385	390	395	
aag aag aca cac aag gat ccg acc tct ggc gac tgg cta aat gca tca				1251
Lys Lys Thr His Lys Asp Pro Thr Ser Gly Asp Trp Leu Asn Ala Ser				
	400	405	410	
tac gtg ttt tac gat gag aat gaa aat ctt gta cgt gtc tac aac cga				1299
Tyr Val Phe Tyr Asp Glu Asn Glu Asn Leu Val Arg Val Tyr Asn Arg				
	415	420	425	
gac tgt gta gac att aat cgg atg gga tat gac tac gaa agg tca gca				1347
Asp Cys Val Asp Ile Asn Arg Met Gly Tyr Asp Tyr Glu Arg Ser Ala				
	430	435	440	
atc cca tgg atc cgt agt cgg ccg act gca cat gcg aag ggg gcg aac				1395
Ile Pro Trp Ile Arg Ser Arg Pro Thr Ala His Ala Lys Gly Ala Asn				
	445	450	460	
gtt gct gct aag tct gct gga atc gtg cag aag gtg gag gat atc gta				1443
Val Ala Ala Lys Ser Ala Gly Ile Val Gln Lys Val Glu Asp Ile Val				
	465	470	475	
ttc ccg ctg aag tta aac aag ata gtg aag gtt cta gtg aag agg cca				1491
Phe Pro Leu Lys Leu Asn Lys Ile Val Lys Val Leu Val Lys Arg Pro				

480	485	490	
gct aca aac agg acc aag gag gga aag gag aaa gca aat gag ctg ttg			1539
Ala Thr Asn Arg Thr Lys Glu Gly Lys Glu Lys Ala Asn Glu Leu Leu			
495	500	505	
ttc gtg aat gga atc acg ttt gat gct gag cgg ttt cta aag att gac			1587
Phe Val Asn Gly Ile Thr Phe Asp Ala Glu Arg Phe Leu Lys Ile Asp			
510	515	520	
gtg ttt gtc aac gac gtc gac gat gga att cag acc acc gct gct gat			1635
Val Phe Val Asn Asp Val Asp Asp Gly Ile Gln Thr Thr Ala Ala Asp			
525	530	535	540
agt gag ttt gct ggt agt ttc gca cag ttg cca cat aac cat ggc gac			1683
Ser Glu Phe Ala Gly Ser Phe Ala Gln Leu Pro His Asn His Gly Asp			
545	550	555	
aag atg ttt atg agg agt ggg gca gcg ttc ggg atc acg gag ctc ttg			1731
Lys Met Phe Met Arg Ser Gly Ala Ala Phe Gly Ile Thr Glu Leu Leu			
560	565	570	
gaa gac att gaa gct gaa ggt gat gac tct gtt gtt gtg aca ttg gtg			1779
Glu Asp Ile Glu Ala Glu Gly Asp Asp Ser Val Val Val Thr Leu Val			
575	580	585	
ccg aga aca ggg tgt gat gaa gta act att ggc gag atc aag att cag			1827
Pro Arg Thr Gly Cys Asp Glu Val Thr Ile Gly Glu Ile Lys Ile Gln			
590	595	600	
ctg gtt ccc att gtt taaagtctat tgaagtaatg catttttcaat tgtcattagt			1882
Leu Val Pro Ile Val			
605			
atgcatgggt acgtaaatct gttcgctgtc tggttatcga ggatttttga tgttctcgta			1942
accaaataat aaggattgtc attccatggt tggaaatcgtg taaccgcagg catgcatatg			2002
tttgattggt atttttactt gaagcacttc tgttttagta aaaaaaaaaa aaaaa			2057

<210> 30

<211> 609

<212> PRT

<213> lettuce

<400> 30

Met	Ala	Ser	Leu	Ala	Leu	Ser	Ser	Leu	Pro	Thr	Ser	Thr	Thr	Thr	Lys	1	5	10	15
Lys	Pro	Leu	Phe	Ser	Lys	Thr	Ser	Ser	His	Val	Lys	Pro	Phe	His	Arg	20	25	30	
Phe	Lys	Val	Ser	Cys	Asn	Ala	Pro	Ala	Asp	Asn	Asn	Asp	Lys	Thr	Val	35	40	45	
Asn	Asn	Ser	Asp	Thr	Pro	Lys	Leu	Ile	Leu	Pro	Lys	Thr	Pro	Leu	Glu	50	55	60	
Thr	Gln	Asn	Val	Asp	Arg	Arg	Asn	Leu	Leu	Leu	Gly	Leu	Gly	Gly	Leu	65	70	75	80
Tyr	Gly	Ala	Ala	Asn	Leu	Thr	Thr	Ile	Pro	Ser	Ala	Phe	Gly	Ile	Pro	85	90	95	
Ile	Ala	Ala	Pro	Asp	Asn	Ile	Ser	Asp	Cys	Val	Ala	Ala	Thr	Ser	Asn	100	105	110	
Leu	Arg	Asn	Ser	Lys	Asp	Ala	Ile	Arg	Gly	Leu	Ala	Cys	Cys	Pro	Pro	115	120	125	
Val	Leu	Ser	Thr	Asn	Lys	Pro	Met	Asp	Tyr	Val	Leu	Pro	Ser	Asn	Pro	130	135	140	
Val	Ile	Arg	Val	Arg	Pro	Ala	Ala	Gln	Lys	Ala	Thr	Ala	Asp	Tyr	Thr	145	150	155	160
Ala	Lys	Tyr	Gln	Gln	Ala	Ile	Gln	Ala	Met	Lys	Asp	Leu	Pro	Glu	Asp	165	170	175	
His	Pro	His	Ser	Trp	Lys	Gln	Gln	Gly	Lys	Ile	His	Cys	Ala	Tyr	Cys	180	185	190	
Asn	Gly	Gly	Tyr	Asn	Gln	Glu	Gln	Ser	Gly	Tyr	Pro	Asn	Leu	Gln	Leu	195	200	205	
Gln	Ile	His	Asn	Ser	Trp	Leu	Phe	Phe	Pro	Phe	His	Arg	Trp	Tyr	Leu	210	215	220	
Tyr	Phe	Tyr	Glu	Lys	Ile	Leu	Gly	Lys	Leu	Ile	Asn	Asp	Pro	Thr	Phe	225	230	235	240
Ala	Leu	Pro	Tyr	Trp	Asn	Trp	Asp	Asn	Pro	Thr	Gly	Met	Val	Ile	Pro	245	250	255	

Ala Met Phe Glu Gln Asn Ser Lys Thr Asn Ser Leu Phe Asp Pro Leu  
260 265 270

Arg Asp Ala Lys His Leu Pro Pro Ser Ile Phe Asp Val Glu Tyr Ala  
275 280 285

Gly Ala Asp Thr Gly Ala Thr Cys Ile Asp Gln Ile Ala Ile Asn Leu  
290 295 300

Ser Ser Met Tyr Arg Gln Met Val Thr Asn Ser Thr Asp Thr Lys Arg  
305 310 315 320

Phe Phe Gly Gly Glu Phe Val Ala Gly Asn Asp Pro Leu Ala Ser Glu  
325 330 335

Phe Asn Val Ala Gly Thr Val Glu Ala Gly Val His Thr Ala Ala His  
340 345 350

Arg Trp Val Gly Asn Ser Arg Met Ala Asn Ser Glu Asp Met Gly Asn  
355 360 365

Phe Tyr Ser Ala Gly Tyr Asp Pro Leu Phe Tyr Val His His Ala Asn  
370 375 380

Val Asp Arg Met Trp Gln Ile Trp Lys Asp Ile Asp Lys Lys Thr His  
385 390 395 400

Lys Asp Pro Thr Ser Gly Asp Trp Leu Asn Ala Ser Tyr Val Phe Tyr  
405 410 415

Asp Glu Asn Glu Asn Leu Val Arg Val Tyr Asn Arg Asp Cys Val Asp  
420 425 430

Ile Asn Arg Met Gly Tyr Asp Tyr Glu Arg Ser Ala Ile Pro Trp Ile  
435 440 445

Arg Ser Arg Pro Thr Ala His Ala Lys Gly Ala Asn Val Ala Ala Lys  
450 455 460

Ser Ala Gly Ile Val Gln Lys Val Glu Asp Ile Val Phe Pro Leu Lys  
465 470 475 480

Leu Asn Lys Ile Val Lys Val Leu Val Lys Arg Pro Ala Thr Asn Arg  
485 490 495

Thr Lys Glu Gly Lys Glu Lys Ala Asn Glu Leu Leu Phe Val Asn Gly  
500 505 510

Ile Thr Phe Asp Ala Glu Arg Phe Leu Lys Ile Asp Val Phe Val Asn  
515 520 525

Asp Val Asp Asp Gly Ile Gln Thr Thr Ala Ala Asp Ser Glu Phe Ala  
530 535 540

Gly Ser Phe Ala Gln Leu Pro His Asn His Gly Asp Lys Met Phe Met  
545 550 555 560

Arg Ser Gly Ala Ala Phe Gly Ile Thr Glu Leu Leu Glu Asp Ile Glu  
565 570 575

Ala Glu Gly Asp Asp Ser Val Val Val Thr Leu Val Pro Arg Thr Gly  
580 585 590

Cys Asp Glu Val Thr Ile Gly Glu Ile Lys Ile Gln Leu Val Pro Ile  
595 600 605

Val

<210> 31

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 31

gcgaattctt yytnccntty mymg

24

<210> 32

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 32

gcgaattcga tccnacntty gckttnc

28

<210> 33

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gcgaattcaa ygtngaymgn atgtgg

26

<210> 34

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34

gcgaattctn caytgygcnt aytg

24

<210> 35

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 35

gcgaattctt nccntwytgg aaytggg

27

<210> 36

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 36

gcctgcagcc acatnckrtc nacrtt

26

<210> 37

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 37

gcctgcagtt ytcrtcrtag aa

22

<210> 38

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 38

gactcgagtc gacatcgatt tttttttttt ttttt

35

<210> 39

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

atatcacctg tcggtacatg acggc

25

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

gtgccattgt agtcgaggtc aatca

25

<210> 41

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

ccagtgcctg gtttaggtgt attcac

26



<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 42

tgctgttctg ttcgaacatg gcag

24

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 43

tatacaagtg gcaccagtgt ctgc

24

<210> 44

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

ccgcattgtg gatgacttcc atctg

25

<210> 45

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

ccagaatggg atggtgaagg tgtcg

25

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